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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/757,093	01/14/2004	Peter Wenzl	415	3522

39124 7590 04/25/2005

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EXAMINER	
MCELWAIN, ELIZABETH F	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 04/25/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/757,093	WENZL, PETER	
	Examiner	Art Unit	
	Maria Teresa Samson	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *04 March 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-30* is/are pending in the application.

4a) Of the above claim(s) *6* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-5 and 7-30* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *16 August 2004* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☒ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *22-March 2004*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Applicant's election with traverse of Group I, claims 1-30, and SEQ ID NO: 3 in the reply filed on 04-March 2005 is acknowledged. The traversal is on the ground(s) that ten sequences constitute a reasonable number for examination purposes, and that up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction. This is not found persuasive. One sequence is "up to ten" and because, given the database size and resource allocation at the USPTO, examination of more than one sequence would present a severe burden on USPTO resources.

Additionally, a protein is not obvious over the polynucleotide that encodes it and that the polynucleotide and the polypeptide are not related because the polynucleotide encodes the polypeptide. The polypeptide is not directly made from the DNA molecule that encodes it. While the nucleic acid sequence may provide researchers the amino acid sequence of the initially-translated protein, it does not allow them to accurately predict properties of the protein like K_m, temperature maximum, or even molecular weight of the processed protein. Additionally, the protein can be isolated from the natural source and characterized in detail without knowledge of the DNA that encodes it, and in fact, many proteins were isolated years before DNA cloning and sequencing were possible. Thus, the protein is not obvious over the nucleic acid that encodes it, and vice versa.

Furthermore, the claims are not limited to single nucleic acid sequences or amino acid sequences, but encompass a multitude of nucleic acid sequence variants encoding a multitude of amino acid sequences with varying properties.

The requirement is still deemed proper and is therefore made FINAL.

Claim 6 and nucleotides 658 to 2580 of SEQ ID NO: 1, nucleotides 736 to 2580 of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, DNA hybridizing to the complement of nucleotides 658 to 2580 of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 and DNA encoding SEQ ID NO: 2, residues 27-641, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, or a variant that has at least 90% amino acid identity to SEQ ID NO: 2, residues 27-641, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 8, or SEQ ID NO: 10 are withdrawn from consideration as being drawn to non-elected inventions.

Claims 31-35 are cancelled.

Claims 1-30 are pending.

Claims 1-5 and 7-30 are examined on the merit that the claims are drawn to SEQ ID NO: 3 encoding SEQ ID NO: 4.

Specification

(A.) The disclosure is objected to because it contains embedded hyperlinks and/or other forms of browser-executable code. See page 40, lines 3 and 7, page 44, lines 7, 15 and 23, page 45, lines 1, 3, and 24, page 46, lines 2 and 24. Applicant is required to delete the embedded hyperlinks and/or other forms of browser-executable code. See MPEP § 608.01.

(B.) The drawings are objected to because figures 10a and b are too dark and no details can be made out.

(C.) The drawings are objected to because figures 10a and b cannot have a brief description on the legends of the figures.

Claim Objections

(A.) Claims 1, 9, 19-27, 29 and 30 are objected to because of the following informalities:

The length of nucleotide sequence of SEQ ID NO: 3 is 1905 bp. However, the claims are drawn to nucleotide sequence of SEQ ID NO: 3 that is 2064 long.

(B.) Claims 1, 2, 8, 9, 19-27, 29 and 30 are objected to for reciting non-elected SEQ ID NOs.

(C.) Claim 29 is objected to because "compliment" line 7 is misspelled.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

(A.) Claims 1-5 and 7-30 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claims contain subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claim is drawn to a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid

molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, the expression vector comprising said DNA, host cells containing the expression vector comprising an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, a method for monitoring expression of a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for transforming a host cell with a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for positive selection for a transformed cell comprising a vector construct comprising a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 encoding a B-fungal glucuronidase with or without a signal peptide and further comprising introducing a vector comprising a nucleic acid sequence encoding a fungal glucuronide transporter and selecting transformed cells transformed, a method of releasing a compound from glucuronide exposed to a host cell expressing B-glucuronidase, a method of monitoring activity of a controller element in a host cell that is transformed with a nucleic acid sequence that hybridizes to the complement of of nucleotides 163 to 2064 of SEQ ID NO: 3 and nucleotides 217 to 2064 of SEQ ID NO: 3 operably linked to a controller element.

Applicant does not describe a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid

molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, the expression vector comprising said DNA, host cells containing the expression vector comprising an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, a method for monitoring expression of a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for transforming a host cell with a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for positive selection for a transformed cell comprising a vector construct comprising a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 encoding a B-fungal glucuronidase with or without a signal peptide and further comprising introducing a vector comprising a nucleic acid sequence encoding a fungal glucuronide transporter and selecting transformed cells transformed, a method of releasing a compound from glucuronide exposed to a host cell expressing B-glucuronidase, a method of monitoring activity of a controller element in a host cell that is transformed with a nucleic acid sequence that hybridizes to the complement of of nucleotides 163 to 2064 of SEQ ID NO: 3 and nucleotides 217 to 2064 of SEQ ID NO: 3 operably linked to a controller element.

Furthermore, there is no functional description of an isolated nucleic acid molecule encoding a fungal B-glucuronidase that would act as a selectable marker for transformation. Applicant does not describe the sufficient structural elements of SEQ ID NO: 3 that are required for function and that these structural elements are also present in nucleic acid molecules that

hybridize to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class. The Applicant does not describe the sufficient structural elements of a representative number of nucleic acids that hybridize to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, and that will hydrolyzed B- glucuronide and will act as a selectable marker for transformation.

Claims 1-5 and 7-30 are rejected under 35 U.S.C. § 112, first paragraph, written description, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Claims 1-5 and 7-30 are drawn to a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, that is claimed solely by function and without any structural limitations.

The Court of Appeals for the Federal Circuit has recently held that a "written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as be structure, formula [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." University of California v. Eli Lilly and Co., 1997 U.S. App. LEXIS 18221, at *23, quoting Fiers v. Revel, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993) (bracketed material in original). To fully describe a genus of genetic material, which is a chemical compound, applicants must (1) fully describe at least one species of the claimed genus sufficient to represent said genus whereby a skilled artisan, in view of the prior art, could predict the structure of other species encompassed by the claimed genus and (2) identify the common characteristics of the claimed molecules, e.g., structure, physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or a combination of these.

In the instant specification, SEQ ID NO: SEQ ID NO: 3 has been set forth, and shown to have B-glucuronidase activity. This DNA sequence is only described according to the functional characteristics of the protein it encodes, for example; no structural relationship is described or used in the claims. Thus, one of skill in the art would be unable to predict the structure of other members of this genus by virtue of the instant disclosure. Therefore, the claims are not adequately described.

Hence, the specification fails to provide an adequate written description of the genus claimed.

Therefore, given the lack of written description in the specification with regard to the structural and functional characteristics of the claimed nucleic acids, it is not clear that Applicant was in possession of the claimed genus at the time this application was filed.

(B.) Claims 1-5 and 7-30 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a rice plant and an E coli transformed with the nucleotides 1 to 1905 of SEQ ID NO: 3 encoding residues 1 to 634 of SEQ ID NO: 4 and said rice plants and E coli express a functional B-glucuronidase, does not reasonably provide enablement for plants, E. coli, insect, cell, fungal cell and an animal cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The claims are drawn to a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, the expression vector comprising said DNA, host cells containing the expression vector

comprising an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, a method for monitoring expression of a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for transforming a host cell with a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for positive selection for a transformed cell comprising a vector construct comprising a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 encoding a B-fungal glucuronidase with or without a signal peptide and further comprising introducing a vector comprising a nucleic acid sequence encoding a fungal glucuronide transporter and selecting transformed cells transformed, a method of releasing a compound from glucuronide exposed to a host cell expressing B-glucuronidase, a method of monitoring activity of a controller element in a host cell that is transformed with a nucleic acid sequence that hybridizes to the complement of of nucleotides 163 to 2064 of SEQ ID NO: 3 and nucleotides 217 to 2064 of SEQ ID NO: 3 operably linked to a controller element.

Applicant's teachings only provide guidance for screening of fungi for expression of B-glucuronidase by growing the fungi on medium containing the glucuronide analog cellobiouronic acid as the sole carbon source (example 1, page 37); confirmation of the isolated fungi express the enzyme GUS and hydrolyze glucuronides (example 2, page 41); cloning of fungal genes (example 3, page 42); sequence analysis of fungal genes and their products (example 4, page 43); identification of additional fungal GUS genes through sequence mining (example 5, page 44);

Expression of either protein, SEQ ID NO: 2 or SEQ ID NO: 4 containing a signal peptide, from E coli and rice plants transformed with the vector comprising either SEQ ID NO: 1 and SEQ ID NO: 3 result in the hydrolyzes of the GUS substrate X-GlcA. Both host cells turn blue in the presence of the GUS substrate X-GlcA (example 6, page 46).

Applicant fails to provide guidance for how to use a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, the expression vector comprising said DNA, host cells containing the expression vector comprising an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class, a method for monitoring expression of a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for transforming a host cell with a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for positive selection for a transformed cell comprising a vector construct comprising a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 encoding a B-fungal glucuronidase with or without a signal peptide and further comprising introducing a vector comprising a nucleic acid sequence encoding a fungal glucuronide transporter and selecting transformed cells transformed, a method of releasing a

compound from glucuronide exposed to a host cell expressing B-glucuronidase, a method of monitoring activity of a controller element in a host cell that is transformed with a nucleic acid sequence that hybridizes to the complement of of nucleotides 163 to 2064 of SEQ ID NO: 3 and nucleotides 217 to 2064 of SEQ ID NO: 3 operably linked to a controller element.

The specification does not teach making a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, or an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class which can hydrolyzed B-glucuronide and can be used to select transformed cells from nontransformed cells.

The specification does not exemplify transforming a plant cell, an insect cell, a fungal cell, an animal cell or a bacterial cell with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4 to select host cells that are transformed from nontransformed cells much less using any an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class with the full scope of the claims and does not teach to make them.

The specification does not exemplify transforming an insect cell, a fungal cell, or an animal cell with SEQ ID NO: 3 encoding SEQ ID NO: 4 or with the nucleotides 163 to 2064 of SEQ ID

NO: 3 in order to select transformed host cells from nontransformed host cells and does not teach to make them.

It is well known to those skilled in the art that making substitutions in a nucleic acid does not produce predictable results. Lazar et al (1988, Mol. Cell. Biol. 8:1247-1252) showed that the "conservative" substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha while "nonconservative" substitutions with alanine or asparagine had no effect (abstract). Similarly, Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach that when three histidines that are maintained in ADP-glucose pyrophosphorylase across several species are substituted with the "nonconservative" amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the "conservative" amino acid arginine drastically reduced enzyme activity (see Table 1).

Given the claim breath, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate B-glucuronidase like genes-encoding nucleic acids that hybridize to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 or encoding a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4. Making all possible single amino acid substitutions in a 634 amino acid long protein like that encoded by SEQ ID NO: 3 would require making and analyzing 19^{634} nucleic acids; these proteins would have 99.8% identity to SEQ ID NO: 4. Because nucleic acids that hybridize to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 or nucleic acids encoding proteins having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4 could encode proteins

with many amino acid substitutions, many more than 19^{634} nucleic acids would need to be made and analyzed. Guo et al. (2004, Proc. Natl. Acad. Sci. USA 101: 9205-9210) teach that while proteins are fairly tolerant to mutations resulting in single amino acid changes, increasing the number of substitutions additively increases the probability that the protein will be inactivated (pg 9209, right column, paragraph 2). Thus, making and analyzing proteins with many amino acid substitutions that also have B-glucuronidase-like activity would require undue experimentation.

Moreover, the specification does not teach how to use the method for monitoring expression of a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for transforming a host cell with a gene of interest in a host cell transformed with a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, a method for positive selection for a transformed cell comprising a vector construct comprising a nucleic acid molecule that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 encoding a B-fungal glucuronidase with or without a signal peptide and further comprising introducing a vector comprising a nucleic acid sequence encoding a fungal glucuronide transporter and selecting transformed cells transformed, a method of releasing a compound from glucuronide exposed to a host cell expressing B-glucuronidase, a method of monitoring activity of a controller element in a host cell that is transformed with a nucleic acid sequence that hybridizes to the complement of of nucleotides 163 to 2064 of SEQ ID NO: 3 and nucleotides 217 to 2064 of SEQ ID NO: 3 operably linked to a controller element.

Additionally, extensive further experimentation would be required to isolate and clone other nucleotide sequence that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, or an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class and to determine whether the sequences can hydrolyzed glucuronides. The specification does not teach where to find such nucleotide sequence that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, or an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class and does not teach how to make them.

Thus, given the limited teachings and guidance by Applicant, the nature of the art and the unpredictability of the art, undue trial and error experimentation would have been required by one of skill in the art at the time of Applicant's invention to use the nucleotide sequence that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, or an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class and to screen through a myriad of nucleotide sequence that hybridizes to the complement of nucleotides 163 to 2064 of SEQ ID NO: 3 which encodes a

functional B-glucuronidase, an isolated nucleic acid molecule that encodes a functional B-glucuronidase having 90% amino acid identity to the residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, or an isolated nucleic acid molecule encoding a fungal B-glucuronidase from the Eurotiomycetes or Sordariomycetes class to find those that are B-glucuronidase -like genes. Therefore, it would require undue experimentation for one skilled in the art to make/or use the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 2, 22, 25 and 29 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Dependent claim is included in all rejections.

(A.) In claim 2, the recitation of "SEQ ID NO: 2, 4, residues 19-634 of SEQ ID NO: 4" is indefinite. It is not clear if applicant meant an isolated nucleic acid molecule that encodes one of the amino acid sequences SEQ ID NO: 4 or residues 19-634 of SEQ ID NO: 4 or SEQ ID NO: 4, residues 19-634.

(B.) Claim 25 recites the limitation "compound is an auxin or a hormone" in line 2. There is insufficient antecedent basis for this limitation in the claim. Claim 21 makes no reference to an auxin or a hormone.

(C.) In claim 9, the recitation of "controller element" is indefinite. It is not clear what is a controller element. It was not defined in the specification.

Conclusion

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maria Teresa Samson whose telephone number is 571-272-3110. The examiner can normally be reached on 7:00-5:00. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

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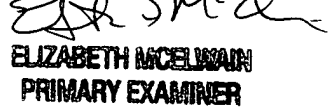
Maria Teresa Samson, Ph.D
April 8, 2005



ELIZABETH MCELWAIN
PRIMARY EXAMINER